5.

56 GCC	110 CCA	164 TCT	218 ATG M	272 GTG V	326 GAA E	380 AAA K	434 CAT H
SCC	TCT	CCC	CTG	ACA T	CTG	AAA C	ATG M
TCT	TCT	CCT	TTG	TTG	, TTA (	CTC	TAT Y
47 , AGA	101 . CTT	155 GGT	209 CGG	263 ACA T	317 GAA E	371 TCC S	425 CAA Q
TGA	AAG	TTC	TAC GAG	GCG A	ATT I	CAA Q	TAT Y
AAC	SSS	CCT	TAC	ATG M	ATG M GCA		GTG
38 CGC	92 CCA	146 CCT	200 CAC	254 GAC D	254 GAC D D 308 AGA R		416 GAG E
CAC	AAC	כנכ	TTT TCT	GCA A GCA A		CAC H	CGA R
500 t	ACC	CCT	TTT	ACG	GTT V	GTG V	ATT
29 A GCT	83 GCT	137 CCT	191 TTT	245 CCC .	299 GAT D	353 CCA P	407 GCT A
TCA	CTG	י ממכ	JCC	TCG GCT S A	AGA R	GTA V	ACA T
) GGC	CAT	CTT	TCC	TCG	GAC	GAA E	TGT C
20 CGA	74 , CTC	128 TTC	182 ATC	236 ACT T	290 CTG L	344 GGA G	398 TTT F
GCA	CGT	TCC	CCA	GTC V	ACC	TCT	GAG E
. TCG	TTG	CCT	CCC	AGC	CTC	GAA E	AGT S
11 1 AAT	65 GCG GAA CAG	119 CCA CCA CCA	173 CCG	227 CTG AAG CCG L K P	281 CCG P	335 CAG Q	389 CAG Q
: AAG	GAA	CCA	CCA CCC	AAG K	GTC CAG V Q	CTA L	CTT
11 GAGGC AAG AAT	909	CCA	CCA	CTG	GTC	AAA CTA K L	GTG CTT O

FIGURE 1A

488	542	596	650	704	758	812
AAG	GTT	GAG	AGA	GTG	AGC	CGC
K	V	E	R	V	S	R
GCA A	GTA V	AAG K	GAA E	AGT S	GAC	GCT G
ACA T	CGA R	GGA		GTG V	AAA K	
479		587	641	695	749	803
GCA		GGA	GTG	GGA	GCT	ATG
A		G	V	G	A	M
AGG	CAC	ATG		AAC	GCT	GAA
R	H	M	G	N	A	E
GCG	TCC	GTG V	GGA G	GTG V	AAG K	GAA E
470	524	578	632	686	740	794
CGT	CAC	AAT	CCT	TCA	CTC	CTG
R	H	N	P	S	L	L
TTC		TTT F	ATT I	CTA L	CTA L	GTT V
GAA	GAA	GGT	ATA	CTG	GAA	AAA
E	E	G	I	L	E	K
461	515	569	623	677	731	785
CCC	AGT	CTT	CGC	CAG	GTG	CCA
P	S	L	R	Q	V	P
TGT	GCT		TCT	GAC D	GCT	ACC
9		GAA	ATC	GGA	AAA	TAC
9		E	I	G	K	Y
452	506	560	614	668	722	776
AAT	TTT	GAT	TAT	AGA	GAG	CGA
N	F	D	Y	R	E	R
GTT V	GCT A	ACT		AAA K		GTG V
ACT T	GCA A	AAG K	CCC	CTC	CAC H	GTG V
443	497	551	605	659	713	767
ATA	GTT	CCA	TCC	GGC	GAA	CTG
I	V	P	S	G	E	L
GAA ACG	ACA	CTG	AAT	GGA	GGA	AAG
E T	T	L	N		G	K
GAA	GCA	GAA E	CAA Q	CAC H	GAA E	GTC V

### FIGURE 1B

866 CAG Q	920 GCC	974 GTG	1028 AAG	1082 TCT	1136	1190	1244 AAA
CTA ATT L I	TCA TAG S	ACC	1028 GTC AAG	1082 CCT TCT	1136 ACC TTC	1190 GTC TGC	1244 AAA AAA
		GAA	CCT	ACA	TTG	CTA	AAA
857 CAA TTG Q L	911 ATG M	965 TTT	1019 ATT ATA	1073 AAC TCA	1127 CAT ACA	1181 GGT TTT	1235 ATA
	CAC H	AAA		1 AAC		1 GGT	1 TAA
848 CAG CAG Q Q	AAC N	CAC	ATA	299	TTA	AGA	1236 TAT GAC TTT TAA ATA
	902 CAA Q	956 AGT	1010 ACA CTG	1064 TAC CAA	1118 TGG GCT	1172 AGA GGG	1226 ' GAC
CGG CAG R Q	CAA Q	GAT			TGG	1 AGA	1 TAT
	893 CAA ACA Q T	TCC	ACA	CTT	ACG	IGC	GTC
839 CGT R		947 ACA	1001 TAA AAG	1055 TAA ATT	1109 CTG CTC	1163 TCA GTG	1208 TGT AAG AAG AAT AAA GTC
AGG R	CAA Q	CAA		TAA	CTG	1 TCA	1 AAT
830 ACA GCC T A	CAG Q	GAT	TAG	GTA	CCA	TTC	AAG
	884 CAG Q	938 CTT	992 ACA	1046 CAT GGT	1100 GAA CCG	1154 TGG GAA	1208 ' AAG
CGA R	CAG Q	CTA	AGC	CAT	GAA	1 TGG	1 TGT
CTA L	CAG Q	AAG	CCC	ACA	CTT	CAG	CAG
821 AAG K	875 CAA Q	929 GGA	983 AAT	1037 TGA	1091 GGG	1145 CTG	1199 3 AAA
821 TTT GAA AAG CTA F E K L	875 CAG CAG CAA CAG Q Q Q	929 CTT GAG GGA AAG	983 CTT CAG AAT	1037 AAG CTG TGA ACA	1091 TTC TCT GGG	1145 CAT TCA CTG	1199 AAA CTG AAA CAG
TTT	CAG Q	CTT	CTT	AAG	TTC	CAT	AAA

### FIGURE 1C

GI 1685067 1974337 LDRDVARAIELLEKLQESGEVPVHKLQSLK LERDVQRILELMEHVQKTGEVNNAKLASLQ 117

GI 1685067 1974337 EFCTAIREVYOYMHETITVNGCPEF EFFGAVREVYETVYESIDADTTPEI KVLQS QVLQS 147

GI 1685067 1974337 LPKT AAAEGHAHPRIVELPKT PRVVE SH E, വ പ A A ഥ VAAF VAAA A T AKAT AK RARAT KAAAT 8 177

GI 1685067 1974337 AD SRIPGGVAE SRIPGGVAD PIYI PIYI DEGLGFNVMGGKEQNS DQGLGFNVMGGKEQNS FNVMGGKE L G DEG 115 207

GI 1685067 1974337 RHGGLKRGDQLLSVNGVSVEGEHHEKAVEL RHGGLKRGDQLIAVNG-NVEAECHEKAVDL 237 145

GI 1685067 1974337 L K A A K D S V K L V V R Y T P K V L E E M E A R F E K L R L K S A V G S V K L V I R Y M P K L L D E M E R R F E R Q R 175 266

#### FIGURE